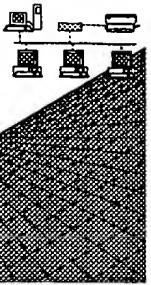


Railey

BIOTECHNOLOGY
SYSTEMS
BRANCH



RAW SEQUENCE LISTING

ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following CRF diskette:

Application Serial Number: 08/846,606A

Art Unit / Team No.: 1636

Date Processed by STIC: 4/14/98

THE ATTACHED PRINTOUT EXPLAINS THE ERRORS DETECTED.

PLEASE BE SURE TO FORWARD THIS INFORMATION TO THE APPLICANTS BY EITHER:

1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANTS ALONG WITH A NOTICE TO COMPLY or,

2) CALLING APPLICANTS AND FAXING THEM A COPY OF THE PRINTOUT WITH A NOTICE TO COMPLY

THIS WILL INSURE THAT THE NEXT SUBMISSION RECEIVED FROM THEM WILL BE ERROR FREE.

IF YOU HAVE ANY FURTHER QUESTIONS, PLEASE CALL:

ARTI SHAH 703-308-4212

Rainer

PAGE: 1

1636

#8 1/2

**RAW SEQUENCE LISTING
PATENT APPLICATION US/08/846,606A**

DATE: 04/14/98
TIME: 13:25:10

INPUT SET: S24919.raw

This Raw Listing contains the General Information Section and those Sequences containing ERRORS.

Does Not Comply
Corrected Diskette Needed

SEQUENCE LISTING

ERRORED SEQUENCES FOLLOW:

106 (2) INFORMATION FOR SEQ ID NO:6:
107 (i) SEQUENCE CHARACTERISTICS:
108 (A) LENGTH: 27 amino acids
109 (B) TYPE: amino acid
110 (ii) MOLECULE TYPE: peptide
111 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:
112
113
114 Asp Asn Asn Leu Ala Gly Ser Gly Ser Gly Asp Asp Asp Asp Lys
115 1 5 10 15
(D) TOPOLOGY: mandatory heading AND response for ALL types of sequences

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/846,606A

INPUT SET: S24919.raw

116
 117 Gly Pro Val Pro Pro Ser Thr Ala Leu Arg Glu Leu
 118 20 25
 119
 120

155 (2) INFORMATION FOR SEQ ID NO:10:

156 (i) SEQUENCE CHARACTERISTICS:

157 (A) LENGTH: 14 bases

158 (B) TYPE: nucleic acid

159 (C) STRANDEDNESS: single

160 (D) TOPOLOGY: linear

161 (ii) MOLECULE TYPE: DNA

--> 162 (xi) SEQUENCE DESCRIPTION: 10: SEQ ID NO:10: (repetitive error)

163
 164 AAGGAGGTTT AATG 14
 165

166 (2) INFORMATION FOR SEQ ID NO:11:

167 (i) SEQUENCE CHARACTERISTICS:

168 (A) LENGTH: 6 amino acids

169 (B) TYPE: amino acid

170 (ii) MOLECULE TYPE: peptide → (D) TOPOLOGY: linear and repeat

--> 171 (xi) SEQUENCE DESCRIPTION: 11: SEQ ID NO:11:

172
 173 Leu Asp Ala Asn Leu Ala
 174 | 5 NUMBER AMINO ACIDS UNDER EVERY 5

⑥ delete

175 (2) INFORMATION FOR SEQ ID NO:12:

176 (i) SEQUENCE CHARACTERISTICS:

arrest
acid

--> 177 (A) LENGTH: 21 bases

178 (B) TYPE: nucleic acid

179 (C) STRANDEDNESS: single

180 (D) TOPOLOGY: linear

181 (ii) MOLECULE TYPE: DNA

--> 182 (xi) SEQUENCE DESCRIPTION: 12:

(DO NOT USE TAB codes-
use space
characters)

184 CTC GAT GCT AAT CTG GCG TAA 21

--> 185 Leu Asp Ala Asn Leu Ala

⑥ delete

186 Misaligned amino acids - Please align them and
 187 number under every 5 amino acids

188 (2) INFORMATION FOR SEQ ID NO:13:

189 (i) SEQUENCE CHARACTERISTICS:

--> 190 (A) LENGTH: 21 bases

191 (B) TYPE: nucleic acid

192 (C) STRANDEDNESS: single

193 (D) TOPOLOGY: linear

194 (ii) MOLECULE TYPE: DNA

--> 195 (xi) SEQUENCE DESCRIPTION: 13:

196 CTC GAG GCT AAT CTG GCG TAA 21

--> 198 Leu Glu Ala Asn Leu Ala

⑥ ✓

align and number them

INPUT SET: S24919.raw

199

200 (2) INFORMATION FOR SEQ ID NO:14:

201 (i) SEQUENCE CHARACTERISTICS:

202 (A) LENGTH: 6 amino acids

203 (B) TYPE: amino acid

204 (ii) MOLECULE TYPE: peptide

--> 205 (xi) SEQUENCE DESCRIPTION:14:

206

207 Leu Glu Ala Asn Leu Ala

208 |

5

209

210

211

↑

↑

6

(D) TOPOLOGY:

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION US/08/846,606A

INPUT SET: S24919.raw

Line	Error	Original Text
111	Wrong or Missing Sequence Topology	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:
162	Mandatory Value Not Present	(xi) SEQUENCE DESCRIPTION SEQ ID NO:10:
171	Mandatory Value Not Present	(xi) SEQUENCE DESCRIPTION SEQ ID NO:11:
171	Wrong or Missing Sequence Topology	(xi) SEQUENCE DESCRIPTION SEQ ID NO:11:
177	Entered (21) and Calc. Seq. Length (32) differ	(A) LENGTH: 21 bases
182	Mandatory Value Not Present	(xi) SEQUENCE DESCRIPTION SEQ ID NO:12:
185	Wrong Nucleic Acid Designator	Leu Asp Ala Asn Leu Ala
185	Wrong Nucleic Acid Designator	Leu Asp Ala Asn Leu Ala
185	Wrong Nucleic Acid Designator	Leu Asp Ala Asn Leu Ala
185	Wrong Nucleic Acid Designator	Leu Asp Ala Asn Leu Ala
185	Wrong Nucleic Acid Designator	Leu Asp Ala Asn Leu Ala
185	Wrong Nucleic Acid Designator	Leu Asp Ala Asn Leu Ala
185	Wrong Nucleic Acid Designator	Leu Asp Ala Asn Leu Ala
185	Wrong Nucleic Acid Designator	Leu Asp Ala Asn Leu Ala
185	# of Sequences for line conflicts w/ running total	Leu Asp Ala Asn Leu Ala
190	Entered (21) and Calc. Seq. Length (32) differ	(A) LENGTH: 21 bases
195	Mandatory Value Not Present	(xi) SEQUENCE DESCRIPTION SEQ ID NO:13:
198	Wrong Nucleic Acid Designator	Leu Glu Ala Asn Leu Ala
198	Wrong Nucleic Acid Designator	Leu Glu Ala Asn Leu Ala
198	Wrong Nucleic Acid Designator	Leu Glu Ala Asn Leu Ala
198	Wrong Nucleic Acid Designator	Leu Glu Ala Asn Leu Ala
198	Wrong Nucleic Acid Designator	Leu Glu Ala Asn Leu Ala
198	Wrong Nucleic Acid Designator	Leu Glu Ala Asn Leu Ala
198	Wrong Nucleic Acid Designator	Leu Glu Ala Asn Leu Ala
198	# of Sequences for line conflicts w/ running total	Leu Glu Ala Asn Leu Ala
205	Mandatory Value Not Present	(xi) SEQUENCE DESCRIPTION SEQ ID NO:14:
205	Wrong or Missing Sequence Topology	(xi) SEQUENCE DESCRIPTION SEQ ID NO:14: